

SEQUENCE LISTING

<110> Biemans, Ralph
 Denoel, Philippe
 Feron, Christiane
 Goraj, Karine
 Kortekaas, Jeroen
 Poolman, Jan
 Tommassen, Jan
 Weynants, Vincent

<120> Mutant Protein and Refolding Method

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<213> Neisseria meningitidis

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<213> Neisseria gonorrhoeae

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<213> *Neisseria meningitidis*

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Phe	Asn	Phe	Asp	Ser	Arg	Leu	Ala	Glu	Gln	Thr	Leu	Leu	Lys	Tyr	Gly	
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Ile	Asn	Tyr	Arg	His	Gln	Glu	Ile	Lys	Pro	Gln	Ala	Phe	Leu	Asn	Ser	
			340					345					350			
Lys	Phe	Ser	Ile	Pro	Thr	Thr	Glu	Lys	Lys	Asn	Gly	Gln	Asp	Val	Ala	
	355						360					365				
Lys	Pro	Ala	Asp	Gln	Gln	Ala	Lys	Asp	Arg	Lys	Asp	Glu	Ala	Leu	Val	
	370					375					380					
His	Ser	Tyr	Arg	Leu	Thr	Asn	Pro	Thr	Lys	Thr	Asp	Thr	Gly	Ala	Tyr	
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Ile	Glu	Ala	Ile	His	Glu	Ile	Asn	Gly	Phe	Thr	Leu	Thr	Gly	Gly	Leu	
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Arg	Tyr	Asp	Arg	Phe	Lys	Val	Lys	Thr	His	Asp	Gly	Lys	Thr	Val	Ser	
			420					425					430			
Ser	Ser	Asn	Leu	Asn	Pro	Ser	Phe	Gly	Val	Ile	Trp	Gln	Pro	His	Glu	
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Gly	Asp	Gly	Thr	Lys	Ala	Glu	Arg	Ala	Arg	Asn	Thr	Glu	Ile	Gly	Phe	
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Asn	Tyr	Asn	Glu	Gly	Thr	Phe	Ala	Ala	Asn	Gly	Arg	Tyr	Phe	Trp	Gln	
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Thr	Ile	Lys	Asp	Ala	Leu	Ala	Asn	Pro	Gln	Asn	Arg	His	Val	Ser	Ala	
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			580					585					590			
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	610					615					620					
Gln	Lys	Asp	Arg	Asn	Gly	Lys	Leu	Glu	Asn	Val	Val	Arg	Lys	Gly	Phe	
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Gly	Val	Asn	Asp	Val	Phe	Ala	Asn	Trp	Lys	Pro	Leu	Gly	Lys	Asp	Thr	
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His	Asn	Val	Asn	Leu	Ser	Val	Asn	Asn	Val	Phe	Asn	Thr	Phe	Tyr	Tyr	
			660					665					670			
Pro	His	Ser	Gln	Arg	Trp	Thr	Asn	Thr	Leu	Pro	Asp	Val	Gly	Arg	Asp	
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<211> 2123
 <212> DNA
 <213> Neisseria meningitidis

<400> 9

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<210> 10
 <211> 692
 <212> PRT
 <213> Neisseria meningitidis

<400> 10

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Lys Asp Glu Ser Thr Ala Thr Asp Met Arg Glu Leu Leu Lys Glu Glu
 35          40          45
Pro Ser Ile Asp Phe Gly Gly Gly Asn Gly Thr Ser Gln Phe Leu Thr
 50          55          60
Leu Arg Gly Met Gly Gln Asn Ser Val Asp Ile Lys Val Asp Asn Ala
 65          70          75          80
Tyr Ser Asp Ser Gln Ile Leu Tyr His Gln Gly Arg Phe Ile Val Asp
 85          90          95
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Pro	Ala	Leu	Val	Lys	Val	Val	Ser	Val	Gln	Lys	Gly	Ala	Gly	Ser	Ala	100	105	110
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Asp	Ala	Gln	Asp	Leu	Leu	Lys	Gly	Leu	Asp	Lys	Asn	Trp	Gly	Val	Arg	130	135	140
Leu	Asn	Ser	Pro	Ser	Asp	Ser	Asn	Glu	Gly	Val	Ser	Tyr	Gly	Ala	Ser	145	150	155
Val	Phe	Gly	Lys	Glu	Gly	Asn	Phe	Asp	Gly	Leu	Phe	Ser	Tyr	Asn	Arg	165	170	175
Asn	Asn	Glu	Lys	Asp	Tyr	Glu	Ala	Gly	Lys	Gly	Phe	Arg	Asn	Asn	Phe	180	185	190
Asn	Gly	Gly	Lys	Thr	Val	Pro	Tyr	Ser	Ala	Leu	Asp	Lys	Arg	Ser	Tyr	195	200	205
Leu	Ala	Lys	Ile	Gly	Thr	Thr	Phe	Gly	Asp	Gly	Asp	His	Arg	Ile	Val	210	215	220
Leu	Ser	His	Met	Lys	Asp	Gln	His	Arg	Gly	Ile	Arg	Thr	Val	Arg	Glu	225	230	235
Glu	Phe	Thr	Val	Gly	Ala	Lys	Asp	Ser	Arg	Ile	Asn	Ile	Lys	Arg	Gln	245	250	255
Val	Pro	Ala	Tyr	Arg	Glu	Thr	Thr	Gln	Ser	Asn	Thr	Asn	Leu	Ala	Tyr	260	265	270
Thr	Gly	Lys	Asn	Leu	Gly	Phe	Val	Glu	Lys	Leu	Asp	Ala	Asn	Ala	Tyr	275	280	285
Val	Leu	Glu	Lys	Glu	Arg	Tyr	Ser	Ala	Asp	Asp	Ser	Gly	Thr	Gly	Tyr	290	295	300
Ala	Gly	Asn	Val	Lys	Gly	Pro	Asn	His	Thr	Arg	Ile	Thr	Thr	Arg	Gly	305	310	315
Ala	Asn	Phe	Asn	Phe	Asp	Ser	Arg	Leu	Ala	Glu	Gln	Thr	Leu	Leu	Lys	325	330	335
Tyr	Gly	Ile	Asn	Tyr	Arg	His	Gln	Glu	Ile	Lys	Pro	Gln	Ala	Phe	Leu	340	345	350
Asn	Ser	Gln	Phe	Lys	Ile	Glu	Asp	Lys	Glu	Lys	Ala	Thr	Asp	Glu	Glu	355	360	365
Lys	Asn	Lys	Asn	Arg	Glu	Asn	Glu	Lys	Ile	Ala	Lys	Ala	Tyr	Arg	Leu	370	375	380
Thr	Asn	Pro	Thr	Lys	Thr	Asp	Ala	Gly	Ala	Tyr	Ile	Glu	Ala	Ile	His	385	390	395
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Lys	Val	Lys	Thr	His	Asp	Gly	Lys	Thr	Val	Ser	Ser	Ser	Asn	Leu	Asn	420	425	430
Pro	Ser	Phe	Gly	Val	Ile	Trp	Gln	Pro	His	Glu	His	Trp	Ser	Phe	Ser	435	440	445
Ala	Ser	His	Asn	Tyr	Ala	Ser	Arg	Ser	Pro	Arg	Leu	Tyr	Asp	Ala	Leu	450	455	460
Gln	Thr	His	Gly	Lys	Arg	Gly	Ile	Ile	Ser	Ile	Ala	Asp	Gly	Thr	Lys	465	470	475
Ala	Glu	Arg	Ala	Arg	Asn	Thr	Glu	Ile	Gly	Phe	Asn	Tyr	Asn	Asp	Gly	485	490	495
Thr	Phe	Ala	Ala	Asn	Gly	Ser	Tyr	Phe	Trp	Gln	Thr	Ile	Lys	Asp	Ala	500	505	510
Leu	Ala	Asn	Pro	Gln	Asn	Arg	His	Asp	Ser	Val	Ala	Val	Arg	Glu	Ala	515	520	525
Val	Asn	Ala	Gly	Tyr	Ile	Lys	Asn	His	Gly	Tyr	Glu	Leu	Gly	Ala	Ser	530	535	540
Tyr	Arg	Thr	Gly	Gly	Leu	Thr	Ala	Lys	Val	Gly	Val	Ser	His	Ser	Lys	545	550	555
Pro	Arg	Phe	Tyr	Asp	Thr	His	Lys	Asp	Lys	Leu	Leu	Ser	Ala	Asn	Pro	565	570	575
Glu	Phe	Gly	Ala	Gln	Val	Gly	Arg	Thr	Trp	Thr	Ala	Ser	Leu	Ala	Tyr			

			580					585					590				
Arg	Phe	Gln	Asn	Pro	Asn	Leu	Glu	Ile	Gly	Trp	Arg	Gly	Arg	Tyr	Val		
		595						600				605					
Gln	Lys	Ala	Val	Gly	Ser	Ile	Leu	Val	Ala	Gly	Gln	Lys	Asp	Arg	Asn		
	610					615					620						
Gly	Lys	Leu	Glu	Asn	Val	Val	Arg	Lys	Gly	Phe	Gly	Val	Asn	Asp	Ile		
625				630					635						640		
Phe	Ala	Asn	Trp	Lys	Pro	Leu	Gly	Lys	Asp	Thr	Leu	Asn	Val	Asn	Leu		
			645						650					655			
Ser	Val	Asn	Asn	Val	Phe	Asn	Thr	Phe	Tyr	Tyr	Pro	His	Ser	Gln	Arg		
		660						665					670				
Trp	Thr	Asn	Thr	Leu	Pro	Asp	Val	Gly	Arg	Asp	Val	Arg	Leu	Gly	Val		
		675					680					685					
Asn	Tyr	Lys	Phe														
	690																

<210> 11
 <211> 16
 <212> PRT
 <213> Neisseria gonorrhoeae

<400> 11
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<210> 12
 <211> 24
 <212> PRT
 <213> Neisseria gonorrhoeae

<400> 12
 Gln His Arg Gly Ile Arg Thr Val Arg Glu Glu Phe Ala Val Ser Glu
 1 5 10 15
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<210> 13
 <211> 23
 <212> PRT
 <213> Neisseria meningitidis

<400> 13
 Asn Gly Gln Asp Val Ala Lys Pro Ala Asp Gln Gln Ala Lys Asp Arg
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<210> 14
 <211> 23
 <212> PRT
 <213> Neisseria meningitidis

<400> 14
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 1 5 10 15
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<210> 15
<211> 16
<212> PRT
<213> Neisseria meningitidis

<400> 15
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<210> 16
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<213> Neisseria meningitidis

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<210> 17
<211> 31
<212> PRT
<213> Neisseria meningitidis

<400> 17
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<210> 18
<211> 29
<212> PRT
<213> Neisseria meningitidis

<400> 18
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<210> 19
<211> 27
<212> PRT
<213> Neisseria meningitidis

<400> 19
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<210> 20

<211> 28
<212> PRT
<213> Neisseria meningitidis

<400> 20
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<210> 21
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Repeat domain of repeat toxin

<221> VARIANT
<222> (1)...(9)
<223> Xaa = Any Amino Acid

<400> 21
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1 5

<210> 22
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Repeat domain of repeat toxin

<221> VARIANT
<222> (1)...(9)
<223> Xaa = Any Amino Acid

<400> 22
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1 5

<210> 23
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Polymyxin B mimotope

<400> 23
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1 5 10

<210> 24
<211> 10
<212> PRT

<213> Artificial Sequence

<220>

<223> Meningococcal PorA p1.7, 16 loop 4 chimera

<400> 24

Gln Leu Lys Asp Thr Asn Asn Asn Ala Ser
1 5 10

<210> 25

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Meningococcal PorA p1.7, 16 loop 4 chimera

<400> 25

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<210> 26

<211> 2135

<212> DNA

<213> Artificial Sequence

<220>

<223> Meningococcal frpB with loop 7 deletion

<400> 26

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<210> 27

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Meningococcal frpB with loop 7 deletion

<400> 27

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          20           25           30
Thr Val Thr Val Lys Gly Asp Arg Gln Gly Ser Lys Ile Arg Thr Asn
          35           40           45
Ile Val Thr Leu Gln Gln Lys Asp Glu Ser Thr Ala Thr Asp Met Arg
          50           55           60
Glu Leu Leu Lys Glu Glu Pro Ser Ile Asp Phe Gly Gly Gly Asn Gly
65          70          75          80
Thr Ser Gln Phe Leu Thr Leu Arg Gly Met Gly Gln Asn Ser Val Asp
          85          90          95
Ile Lys Val Asp Asn Ala Tyr Ser Asp Ser Gln Ile Leu Tyr His Gln
          100         105         110
Gly Arg Phe Ile Val Asp Pro Ala Leu Val Lys Val Val Ser Val Gln
          115         120         125
Lys Gly Ala Gly Ser Ala Ser Ala Gly Ile Gly Ala Thr Asn Gly Ala
          130         135         140
Ile Ile Ala Lys Thr Val Asp Ala Gln Asp Leu Leu Lys Gly Leu Asp
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Lys Asn Trp Gly Val Arg Leu Asn Ser Gly Phe Ala Ser Asn Glu Gly
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Val Ser Tyr Gly Ala Ser Val Phe Gly Lys Glu Gly Asn Phe Asp Gly
          180         185         190
Leu Phe Ser Tyr Asn Arg Asn Asp Glu Lys Asp Tyr Glu Ala Gly Lys
          195         200         205
Gly Phe Arg Asn Val Asn Gly Gly Lys Thr Val Pro Tyr Ser Ala Leu
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Asp Lys Arg Ser Tyr Leu Ala Lys Ile Gly Thr Thr Phe Gly Asp Asp
225         230         235         240
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          245         250         255
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Asn Ile Asp Arg Gln Ala Pro Ala Tyr Arg Glu Thr Thr Gln Ser Asn
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Thr Asn Leu Ala Tyr Thr Gly Lys Asn Leu Gly Phe Val Glu Lys Leu
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Asp Ala Asn Ala Tyr Val Leu Glu Lys Glu Arg Tyr Ser Ala Asp Asp
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Ser Gly Thr Gly Tyr Ala Gly Asn Val Lys Gly Pro Asn His Thr Arg
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aagagggcaa cttcgacggc ttgttctctt acaaccgcaa cgatgaaaaa gattacgaag 660
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acaagttcta aaacgcacga cgt 2063

```

<210> 29

<211> 668

<212> PRT

<213> Artificial Sequence

<220>

<223> Meningococcal FrpB with loop 7 and 5 deletion

<400> 29

```

Met Asn Thr Pro Leu Phe Arg Leu Ser Leu Leu Ser Leu Thr Leu Ala
1          5          10          15
Ala Gly Phe Ala His Ala Ala Glu Asn Asn Ala Lys Val Val Leu Asp
20          25          30
Thr Val Thr Val Lys Gly Asp Arg Gln Gly Ser Lys Ile Arg Thr Asn
35          40          45
Ile Val Thr Leu Gln Gln Lys Asp Glu Ser Thr Ala Thr Asp Met Arg
50          55          60
Glu Leu Leu Lys Glu Glu Pro Ser Ile Asp Phe Gly Gly Gly Asn Gly
65          70          75          80
Thr Ser Gln Phe Leu Thr Leu Arg Gly Met Gly Gln Asn Ser Val Asp
85          90          95
Ile Lys Val Asp Asn Ala Tyr Ser Asp Ser Gln Ile Leu Tyr His Gln
100         105         110
Gly Arg Phe Ile Val Asp Pro Ala Leu Val Lys Val Val Ser Val Gln
115         120         125
Lys Gly Ala Gly Ser Ala Ser Ala Gly Ile Gly Ala Thr Asn Gly Ala
130         135         140
Ile Ile Ala Lys Thr Val Asp Ala Gln Asp Leu Leu Lys Gly Leu Asp

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145					150					155					160
Lys	Asn	Trp	Gly	Val	Arg	Leu	Asn	Ser	Gly	Phe	Ala	Ser	Asn	Glu	Gly
				165					170					175	
Val	Ser	Tyr	Gly	Ala	Ser	Val	Phe	Gly	Lys	Glu	Gly	Asn	Phe	Asp	Gly
			180					185					190		
Leu	Phe	Ser	Tyr	Asn	Arg	Asn	Asp	Glu	Lys	Asp	Tyr	Glu	Ala	Gly	Lys
		195					200				205				
Gly	Phe	Arg	Asn	Val	Asn	Gly	Gly	Lys	Thr	Val	Pro	Tyr	Ser	Ala	Leu
	210					215				220					
Asp	Lys	Arg	Ser	Tyr	Leu	Ala	Lys	Ile	Gly	Thr	Thr	Phe	Gly	Asp	Asp
225					230					235					240
Asp	His	Arg	Ile	Val	Leu	Ser	His	Met	Lys	Asp	Arg	Gln	Ala	Pro	Ala
				245					250					255	
Tyr	Arg	Glu	Thr	Thr	Gln	Ser	Asn	Thr	Asn	Leu	Ala	Tyr	Thr	Gly	Lys
			260					265					270		
Asn	Leu	Gly	Phe	Val	Glu	Lys	Leu	Asp	Ala	Asn	Ala	Tyr	Val	Leu	Glu
		275					280					285			
Lys	Glu	Arg	Tyr	Ser	Ala	Asp	Asp	Ser	Gly	Thr	Gly	Tyr	Ala	Gly	Asn
	290					295					300				
Val	Lys	Gly	Pro	Asn	His	Thr	Arg	Ile	Thr	Thr	Arg	Gly	Ala	Asn	Phe
305					310					315					320
Asn	Phe	Asp	Ser	Arg	Leu	Ala	Glu	Gln	Thr	Leu	Leu	Lys	Tyr	Gly	Ile
				325				330						335	
Asn	Tyr	Arg	His	Gln	Glu	Ile	Lys	Pro	Gln	Ala	Phe	Leu	Asn	Ser	Lys
			340				345						350		
Phe	Ser	Ile	Pro	Ala	Tyr	Lys	Leu	Ser	Asn	Pro	Thr	Lys	Thr	Asp	Thr
	355					360						365			
Gly	Val	Tyr	Val	Glu	Ala	Ile	His	Asp	Ile	Gly	Asp	Phe	Thr	Leu	Thr
	370					375					380				
Gly	Gly	Leu	Arg	Tyr	Asp	Arg	Phe	Lys	Val	Lys	Thr	His	Asp	Gly	Arg
385					390					395					400
Thr	Val	Ser	Ser	Ser	Asn	Leu	Asn	Pro	Ser	Phe	Gly	Val	Ile	Trp	Gln
				405				410						415	
Pro	His	Glu	His	Trp	Ser	Phe	Ser	Ala	Ser	His	Asn	Tyr	Ala	Ser	Arg
			420				425						430		
Ser	Pro	Arg	Leu	Tyr	Asp	Ala	Leu	Gln	Thr	His	Gly	Lys	Arg	Gly	Ile
		435					440					445			
Ile	Ser	Ile	Ala	Asp	Gly	Thr	Lys	Ala	Glu	Arg	Ala	Arg	Asn	Thr	Glu
	450					455					460				
Ile	Gly	Phe	Asn	Tyr	Asn	Asp	Gly	Thr	Phe	Ala	Ala	Asn	Gly	Ser	Tyr
465					470					475					480
Phe	Trp	Gln	Thr	Ile	Lys	Asp	Ala	Leu	Ala	Asn	Pro	Gln	Asn	Arg	His
				485				490						495	
Asp	Ser	Val	Ala	Val	Arg	Glu	Ala	Val	Asn	Ala	Gly	Tyr	Ile	Lys	Asn
			500					505					510		
His	Gly	Tyr	Glu	Leu	Gly	Ala	Ser	Tyr	Arg	Thr	Gly	Gly	Leu	Thr	Ala
		515					520					525			
Lys	Val	Gly	Val	Ser	His	Ser	Lys	Pro	Arg	Phe	Tyr	Asp	Thr	His	Lys
	530					535					540				
Asp	Lys	Leu	Leu	Ser	Ala	Asn	Pro	Glu	Phe	Gly	Ala	Gln	Val	Gly	Arg
545					550					555					560
Thr	Trp	Thr	Ala	Ser	Leu	Ala	Tyr	Arg	Phe	Gln	Asn	Pro	Asn	Leu	Glu
				565				570						575	
Ile	Gly	Trp	Arg	Gly	Arg	Tyr	Val	Gln	Lys	Ala	Thr	Gly	Ser	Ile	Leu
			580				585					590			
Ala	Ala	Gly	Gln	Lys	Asp	Arg	Lys	Gly	Asn	Leu	Glu	Asn	Val	Val	Arg
		595					600					605			
Lys	Gly	Phe	Gly	Val	Asn	Asp	Val	Phe	Ala	Asn	Trp	Lys	Pro	Leu	Gly
	610					615					620				
Lys	Asp	Thr	Leu	Asn	Val	Asn	Leu	Ser	Val	Asn	Asn	Val	Phe	Asn	Lys
625					630					635					640

<220>

<223> Meningococcal frpB with inner-core LOS binding
sequence (EVLFRGT) built into a loop

<400> 31

Met	Asn	Thr	Pro	Leu	Phe	Arg	Leu	Ser	Leu	Leu	Ser	Leu	Thr	Leu	Ala
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Ala	Gly	Phe	Ala	His	Ala	Ala	Glu	Asn	Asn	Ala	Lys	Val	Val	Leu	Asp
			20					25					30		
Thr	Val	Thr	Val	Lys	Gly	Asp	Arg	Gln	Gly	Ser	Lys	Ile	Arg	Thr	Asn
		35					40					45			
Ile	Val	Thr	Leu	Gln	Gln	Lys	Asp	Glu	Ser	Thr	Ala	Thr	Asp	Met	Arg
	50					55					60				
Glu	Leu	Leu	Lys	Glu	Glu	Pro	Ser	Ile	Asp	Phe	Gly	Gly	Gly	Asn	Gly
65					70					75				80	
Thr	Ser	Gln	Phe	Leu	Thr	Leu	Arg	Gly	Met	Gly	Gln	Asn	Ser	Val	Asp
			85						90					95	
Ile	Lys	Val	Asp	Asn	Ala	Tyr	Ser	Asp	Ser	Gln	Ile	Leu	Tyr	His	Gln
			100					105					110		
Gly	Arg	Phe	Ile	Val	Asp	Pro	Ala	Leu	Val	Lys	Val	Val	Ser	Val	Gln
		115					120					125			
Lys	Gly	Ala	Gly	Ser	Ala	Ser	Ala	Gly	Ile	Gly	Ala	Thr	Asn	Gly	Ala
	130					135					140				
Ile	Ile	Ala	Lys	Thr	Val	Asp	Ala	Gln	Asp	Leu	Leu	Lys	Gly	Leu	Asp
145					150					155				160	
Lys	Asn	Trp	Gly	Val	Arg	Leu	Asn	Ser	Gly	Phe	Ala	Ser	Asn	Glu	Gly
			165						170					175	
Val	Ser	Tyr	Gly	Ala	Ser	Val	Phe	Gly	Lys	Glu	Gly	Asn	Phe	Asp	Gly
			180					185					190		
Leu	Phe	Ser	Tyr	Asn	Arg	Asn	Asp	Glu	Lys	Asp	Tyr	Glu	Ala	Gly	Lys
		195					200					205			
Gly	Phe	Arg	Asn	Val	Asn	Gly	Gly	Lys	Thr	Val	Pro	Tyr	Ser	Ala	Leu
	210					215					220				
Asp	Lys	Arg	Ser	Tyr	Leu	Ala	Lys	Ile	Gly	Thr	Thr	Phe	Gly	Asp	Asp
225					230					235				240	
Asp	His	Arg	Ile	Val	Leu	Ser	His	Met	Lys	Asp	Gln	His	Arg	Gly	Ile
			245						250					255	
Arg	Thr	Val	Arg	Glu	Glu	Phe	Thr	Val	Gly	Asp	Lys	Ser	Ser	Arg	Ile
		260						265					270		
Asn	Ile	Asp	Arg	Gln	Ala	Pro	Ala	Tyr	Arg	Glu	Thr	Thr	Gln	Ser	Asn
	275					280						285			
Thr	Asn	Leu	Ala	Tyr	Thr	Gly	Lys	Asn	Leu	Gly	Phe	Val	Glu	Lys	Leu
290					295						300				
Asp	Ala	Asn	Ala	Tyr	Val	Leu	Glu	Lys	Glu	Arg	Tyr	Ser	Ala	Asp	Asp
305					310					315				320	
Ser	Gly	Thr	Gly	Tyr	Ala	Gly	Asn	Val	Lys	Gly	Pro	Asn	His	Thr	Arg
			325						330					335	
Ile	Thr	Thr	Arg	Gly	Ala	Asn	Phe	Asn	Phe	Asp	Ser	Arg	Leu	Ala	Glu
		340					345						350		
Gln	Thr	Leu	Leu	Lys	Tyr	Gly	Ile	Asn	Tyr	Arg	His	Gln	Glu	Ile	Lys
	355					360						365			
Pro	Gln	Ala	Phe	Leu	Asn	Ser	Lys	Phe	Ser	Ile	Pro	Thr	Thr	Glu	Glu
	370				375						380				
Lys	Asn	Gly	Gln	Lys	Val	Asp	Glu	Val	Leu	Phe	Arg	Gly	Thr	Lys	Pro
385					390					395				400	
Met	Glu	Gln	Gln	Met	Lys	Asp	Arg	Ala	Asp	Glu	Asp	Thr	Val	His	Ala
			405						410					415	
Tyr	Lys	Leu	Ser	Asn	Pro	Thr	Lys	Thr	Asp	Thr	Gly	Val	Tyr	Val	Glu
		420					425					430			
Ala	Ile	His	Asp	Ile	Gly	Asp	Phe	Thr	Leu	Thr	Gly	Gly	Leu	Arg	Tyr

[illegible]